Jennifer J. Barb **(w) 301-435-9232**
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EDUCATION

Ph.D. Bioinformatics May 2009
George Mason University, Manassas, VA

M.S. Biotechnology with concentration in Bioinformatics May 2003
Johns Hopkins University, Rockville, MD

B.S. Computer and Information Science August 2001
University of Maryland University College, Adelphi, MD

B.S. Biological Science May 1999
University of Maryland Baltimore County, Catonsville, MD

RESEARCH INTERESTS

Gene expression analysis, alternative splicing analysis using exon microarrays, next-gen sequencing methods and techniques, data mining, bioinformatics methods, public annotation sources

WORK HISTORY

NIH, Center for Information Technology, Division of Computational Biosciences, Bethesda, MD
May 2001 - present
Working as a bioinformatics consultant on microarray data analysis. Duties include collaborating with intramural staff in analyzing microarray data, preparing figures for publication, maintaining lab's microarray analysis package (MSCL Analyst's Toolbox) written in JMP scripting language (JSL), maintaining annotation data for Affymetrix gene chips, assisting with bioinformatics projects. Developed software (GO-SCAN) that analyzes the significance of gene ontology annotations to a given gene list resulted from standard statistical analysis techniques. Developed packaged to analyze exon microarray data. Teach a course for CIT biannually titled Analyzing microarray data using the MSCL Analyst's Toolbox.

USDA, Agricultural Research Service: Soybean and Alfalfa Research Lab, Beltsville, MD
September 1998 - February 1999
Worked as a biological lab technician. Duties included running gel electrophoresis preps, DNA extraction, using the spectrophotometer, electroporation, PCR, maintaining nematode cell line. Computer activities included running BLAST, organizing sequence data, working with Excel spreadsheets.

UMBC, The Laboratory of Dr. Terry Viancour, Ph.D. of Neurophysiology, Baltimore, MD
August 1998 - May 1999
Worked as biology lab student in an on campus lab. Participated in the construction of an electric fish localization apparatus for a 60 gallon fish tank. Studied the localization of an electric fish using a neural-net information system and collaborated with bioinformatics professor on campus, Jim O'Neill. Participated in a two week research project in Venezuela researching new species of electric fish. Presented relevant work at an Undergraduate Research Symposium, Spring 1999.

PhD DISSERTATION ABSTRACT

Elucidating splice variants using the Affymetrix exon array: Effective probeset filtering is essential. Abstract: Alternative splicing (AS) of mRNA is a major source of diversity of gene products in mammalian genomes, and is a part of a cell's programmed response to its environment in development or disease. The Affymetrix Human Exon 1.0 ST Array measures expression of ~10^6 individual exons, allowing screening for potential splice variants. Data analysis for this platform is complex and problematic because of certain data artifacts. The conventional ANOVA model for Exon Array data includes factors for: Treatment effect; Variation within treatment group; Exon-specific probeset effect; and Treatment-Exon interaction. For the exons contained in each gene, this three-factor, mixed effect model is fit to transformed data and the significance and magnitude of the treatment-exon interaction is interpreted as evidence for AS. We have identified several shortcomings of this approach. Annotations (groupings of exons into genes) may be incorrect, grouping several distinct genes into one. Exons themselves may be incorrectly annotated. Low-intensity ("dead") probesets may not hybridize with their intended target. Surprisingly, many high-intensity probesets may also be unresponsive to treatment, possibly due to cross-hybridization. Each of these may contribute to false identification of AS. We assessed the severity of each problem with the following steps. The Exon array was re-annotated, based on the conservatively defined RefSeq genes database. "Non-core" exons were excluded. Low-intensity probesets were identified and removed. Unresponsive probesets showing low variation across a wide variety of conditions in several datasets were excluded. We illustrate the benefits of this approach in screening for AS in the Affymetrix tissue data set from 11 human tissues. The data are available at www.affymetrix.com.

PEER-REVIEWED PUBLICATIONS

- Strunnikova NV, Barb J, Sergeev YV, Thiagarajasubramanian A, Silvin C, Munson PJ, Macdonald IM. Loss-of-function mutations in Rab escort protein 1 (REP-1) affect intracellular transport in fibroblasts and monocytes of choroideremia patients. PLoS One. 2009 Dec 22.
- Chhikara M, Wang S, Kern SJ, Ferreyra GA, Barb JJ, Munson PJ, Danner RL. Carbon monoxide blocks lipopolysaccharide-induced gene expression by interfering with proximal TLR4 to NF-kappaB signal transduction in human monocytes. *PLoS One*. 2009 Dec 2.
- Deans KJ, Minneci PC, Chen H, Kern SJ, Logun C, Alsaaty S, Norsworthy KJ, Theel SM, Sennesh JD, Barb JJ, Munson PJ, Danner RL, Solomon MA., Impact of animal strain on gene expression in a rat model of acute cardiac rejection. *BMC Genomics*. 2009 Jun 24.
- Hernandez-Novoa B, Bishop L, Logun C, Munson PJ, Elnekave E, Rangel ZG, Barb J, Danner RL, Kovacs JA., Immune responses to Pneumocystis murina are robust in healthy mice but largely absent in CD40 ligand-deficient mice. *J Leukoc Biol*. 2008 May 8.
- Woszczek G, Chen LY, Nagineni S, Kern S, Barb J, Munson PJ, Logun C, Danner RL, Shelhamer JH., Leukotriene D(4) induces gene expression in human monocytes through cysteinyl leukotriene type I receptor. *J Allergy Clin Immunol*. 2008 Jan;121(1):215-221
- Elshal MF, Khan SS, Raghavachari N, Takahashi Y, Barb J, Bailey JJ, Munson PJ, Solomon MA, Danner RL, McCoy JP Jr., A unique population of effector memory lymphocytes identified by CD146 having a distinct immunophenotypic and genomic profile. *BMC Immunol*. 2007 Nov 13;8:29.
- Oliveira JB, Bidère N, Niemela JE, Zheng L, Sakai K, Nix CP, Danner RL, Barb J, Munson PJ, Puck JM, Dale J, Straus SE, Fleisher TA, Lenardo MJ., NRAS mutation causes a human

autoimmune lymphoproliferative syndrome. *Proc Natl Acad Sci U S A*. 2007 May 22;104(21):8953-8.

- Cleary S, Phillips JK, Huynh TT, Pacak K, Elkahloun AG, Barb J, Worrell RA, Goldstein DS, Eisenhofer G., Neuropeptide Y expression in phaeochromocytomas: relative absence in tumours from patients with von Hippel-Lindau syndrome. *J Endocrinol*. 2007 May;193(2):225-33.
- Raghavachari N, Xu X, Harris A, Villagra J, Logun C, Barb J, Solomon MA, Suffredini AF, Danner RL, Kato G, Munson PJ, Morris SM Jr, Gladwin MT., Amplified expression profiling of platelet transcriptome reveals changes in arginine metabolic pathways in patients with sickle cell disease. *Circulation*. 2007 Mar 27; 115(12):1551-62. Epub 2007 Mar 12.
- Brouwers FM, Elkahloun AG, Munson PJ, Eisenhofer G, Barb J, Linehan WM, Lenders JW, DE Krijger R, Mannelli M, Udelsman R, Ocal IT, Shulkin BL, Bornstein SR, Breza J, Ksinantova L, Pacak K: Gene expression profiling of benign and malignant pheochromocytoma. *Ann N Y Acad Sci*. 2006 Aug;1073:541-56
- Wang S, Zhang J, Theel S, Barb JJ, Munson PJ, Danner RL, Nitric oxide activation of Erk1/2 regulates the stability and translation of mRNA transcripts containing CU-rich elements. *Nucleic Acids Res*. 2006 Jun 6;34(10):3044-56. Print 2006.
- Talwar S, Munson PJ, Barb JJ, Fiuza C, Cintron AP, Logun C, Tropea J, Khan S, Reda D, Shelhamer JH, Danner RL, Suffredini AF, Gene expression profiles of peripheral blood leukocytes after endotoxin challenge in humans. *Physiol Genomics*. 2006 Apr 13;25(2):203-15. Epub 2006 Jan 10.
- Cui X, Zhang J, Ma P, Myers DE, Goldberg IG, Sittler KJ, Barb JJ, Munson PJ, Cintron Adel P, McCoy JP, Wang S, Danner RL, cGMP-independent nitric oxide signaling and regulation of the cell cycle. *BMC Genomics*. 2005 Nov 3;6:151.
- Pawliczak R, Logun C, Madara P, Barb J, Suffredini AF, Munson PJ, Danner RL, Shelhamer JH, Influence of IFN-gamma on gene expression in normal human bronchial epithelial cells: modulation of IFN-gamma effects by dexamethasone. *Physiol Genomics*. 2005 Sep 21;23(1):28-45. Epub 2005 Jun 28.
- Jison ML, Munson PJ, Barb JJ, Suffredini AF, Talwar S, Logun C, Raghavachari N, Beigel JH, Shelhamer JH, Danner RL, and Gladwin ML: Blood mononuclear cell gene expression profiles characterize the oxidant, hemolytic and inflammatory stress of sickle cell disease. *Blood*, July 2004.

PRESENTATIONS

- Barb JJ, Munson PJ: Tissue specific alternative splicing on the Affymetrix Human 1.0 ST array using the MSCL Analyst's toolbox. *The NIH Research Festival*, poster, Oct 2009
- Probeset quality hinders analysis of Affymetrix exon data: Improved filters are effective. *ISMB2008*, poster, Toronto, Canada, August 2008
- Barb JJ, Wang S, Ferreyra G, Kern S, Bailey JJ, Danner RL, Solka J and Munson PJ. Statistical and Bioinformatics Filters for Interpretation of Affymetrix Exon Array: LPS effect on THP1cells. FGC2007: Forging a Critical Alliance: Are We Meeting the Need?, poster, Bethesda, MD November 2007
- Barb JJ and Munson PJ. MSCL Toolbox analysis of gene expression: Inflammation response to endotoxin. JMP Discovery 2008, poster, Cary, NC. July 2008

- Barb JJ, Munson PJ: The MSCL Analyst's Toolbox: A powerful analysis package for Microarray Data. *Functional Genomics and Critical Illness and Injury: Surviving Stress*, poster, Bethesda, MD, November 13-14, 2006
- Barb JJ, Munson PJ: The MSCL Analyst's Toolbox: A powerful analysis package for Microarray Data. *NIH Research Festival 2006*, poster, Bethesda, MD October 2006
- Barb JJ, Munson PJ: The MSCL Analyst's Toolbox: A powerful analysis package for Microarray Data. *Microarray Data Analysis and Interpretation*, poster, Washington DC, April 23-25, 2006
- Barb JJ, Schindel H, Munson PJ: GO-SCAN: analysis and visualization of Gene Ontology annotations, Gene Ontology Significant Collection of Annotations. *NIH Research Festival 2004*, poster, Bethesda, MD. September 2004.

LECTURES AND RELATED ACTIVITIES

- Gene and Exon Microarray Analysis, Georgetown University, Washington DC, 1 class taught (invited). Graduate level students. March 2010
- Guest Biomedical Judge at Patriots Technical Training Center, Biomedical Competition, Landover, MD. Jan 2010
- Gene Expression Analysis, George Mason University, 1 class taught (invited). Graduate level students. November 2008
- Member of the Board of Directors, Mid-Atlantic JMP User's Group (MAJUG), Treasurer. September 2008-present
- Bioinformatics Colloquium, 1 lecture (invited). Graduate level students. December 2009
- The analysis of gene expression data using the MSCL Analyst's Toolbox. CIT Training Courses at the NIH. Bethesda, MD. Apr 2004, Nov 2004, Mar 2005, Nov 2006, Mar 2008, Jun 2009